INTISARI

APRILLA, D.U.S., 2014, ANALISIS *DOCKING* MOLEKULER SENYAWA TURUNAN 3-AMINOPIRIDIN-2(1H)-ON TERHADAP ENZIM *REVERSE TRANSCRIPTASE* HIV-1, SKRIPSI, FAKULTAS FARMASI, UNIVERSITAS SETIA BUDI, SURAKARTA.

Enzim *reverse transcriptase* (RT) adalah salah satu enzim penting pada siklus hidup *human immunodeficiency virus* (HIV). Salah satu penghambat enzim RT adalah golongan *non-nucleoside reverse transcriptase* (NNRTI) yaitu turunan piridinon yang menghambat secara non-kompetitif. Pada penelitian ini dilakukan *docking* untuk mengetahui pola interaksi senyawa dan korelasi antara data IC_{50} 26 senyawa turunan 3-aminopiridin-2(1H)-on dan data energi bebas (ΔG) pada proses *docking*.

Proses *docking* diawali dengan membuat struktur 2D 26 turunan piridinon dan dioptimasi dengan program HyperChem. Protein target diambil dari file *protein data bank* (*pdb*) 2BE2 dan dipreparasi. Validasi menghasilkan nilai *root mean square deviation* <2Å. *Docking* menggunakan AutoDock Vina. Hasil *docking* ditampilkan dalam program PyMol.

Ada empat daerah penghambatan pada penelitian ini dan yang paling dominan berada pada daerah penghambatan yang sama dengan daerah penghambatan ligan asli. Asam amino yang terlibat dalam daerah penghambatan ligan asli adalah Leu100A, Lys103A, Val106A, Tyr 188A, Phe227A, Trp229A, Leu234A, His235A, Pro236A, dan Pro96A yang merupakan interaksi hidrofobik dan ada interaksi hidrogen dengan Lys101A. Afinitas senyawa yang ditunjukkan dengan nilai ΔG memberikan nilai pengikatan pada protein target yang cukup kuat (-5 sampai -10 kkal/mol). Pada penetian ini ΔG tidak berkorelasi dengan IC_{50} karena adanya afinitas harus diikuti dengan aktivitas intrinsik untuk menimbulkan efek.

Kata kunci: HIV, Human Immunodeficiency Virus; Reverse transcriptase, RT; NNRTI, *non-nucleoside reverse transcriptase*; Antiviral; 3-aminopiridin-2(1H)-on: docking.

ABSTRACT

APRILLA, D.U.S., 2014, ANALYSIS MOLECULAR DOCKING OF 3-AMINOPIRIDIN-2(1H)-ON DERIVATIVES TOWARD REVERSE TRANSCRIPTASE ENZIME HIV-1, UNDERGRADUATE THESIS, PHARMACY FACULTY, SETIA BUDI UNIVERSITY, SURAKARTA.

Reverse transcriptase (RT) is an essential enzyme for the human immunodeficiency virus (HIV) life cyle. One class of the anti-HIV is non-nucleoside reverse transcriptase inhibitors (NNRTIs), i.e pyridinone derivatives which is non-competitive inhibitors. 3-aminopyridin-2(1H)-one derivatives were docked to see interaction between the compounds and to know the correlation of IC_{50} data of 3-aminopyridin-2(1H)-one derivatives with the binding energy from docking process.

For starting docking, 2D structure of 26 piridinone derivatives was made and optimized using Hyperchem. Protein target were downloaded from protein data bank (pdb) 2BE2 and was prepared. For validated, the calculation root mean square deviation (RMSD) must be less than 2Å. AutoDock Vina was used to docking. All analysis docking results were obtained using PyMol.

There were four inhibition cluster and the dominant cluster was same with the inhibition cluster of ligand. The residue in the inhibition cluster ligand was Leu100A, Lys103A, Val106A, Tyr188A, Phe227A, Trp229A, Leu234A, His235A, Pro236A, and Pro96A which had hidrophobic interaction and the hydrogen interaction with Lys101A. The affinity were representated as ΔG binding (-5 till -10 kcal/mol), showed that adequate strong. In this research, ΔG didn't corelate with IC_{50} due to the affinity be followed by the intrinsic activity for obtain the efficacy.

Keywords: HIV, Human Immunodeficiency Virus; Reverse transcriptase, RT; NNRTI, non-nucleoside reverse transcriptase; Antiviral; 3-aminopiridin-2(1H)-on: docking